

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Application of: Berka *et al.*

Confirmation No. 6980

Serial No.: 09/533,559

Group Art Unit: 1631

Filed: March 22, 2000

Examiner: J.S. Brusca

For: Methods For Monitoring Multiple Gene Expression

DECLARATION UNDER 37 C.F.R. § 1.132

Commissioner for Patents
Washington, DC 20231

Sir:

I, Randy Berka, do hereby state and declare that

1. I am one of the inventors of the subject matter disclosed and claimed in the above-captioned application.
2. I received a Ph.D. in Microbiology and Immunology from the University of Colorado, Health Science Center, Denver, Colorado, in 1983. I have been employed at Novozymes Biotech, Inc., Davis, California, since 1992 where I am currently a Research Fellow.
3. I have read the Office Action dated November 7, 2002 and the Advisory Action dated May 22, 2003 issued in connection with the above-referenced patent application and understand that claims 103-110 have been rejected under 35 U.S.C. § 101 as not supported by a substantial utility. I respectfully disagree with this conclusion.
4. Using Applicants' disclosure in the above-captioned application, one of ordinary skill in the art would be able to set-up and use the methods of the present invention to monitor global expression of a plurality of genes from a filamentous fungal cell with respect to a particular phenotype such as improved secretion or production of a protein or compound, reduced or no secretion or production of a protein or compound, improved or reduced expression of a gene or pathway, desirable morphology, an altered growth rate under desired conditions, relief of over-expression mediated growth inhibition, or tolerance to low oxygen conditions; to discover new genes; to identify possible functions of unknown open reading frames; and to monitor gene copy number variation and stability. For example, the global view of changes in expression of genes may be used to provide a picture of the way in which filamentous fungal cells adapt to changes in culture conditions, environmental stress, or other physiological provocation. Applicants also

provide other possibilities for monitoring global expression including spore formation/germination, recombination, metabolic or catabolic pathway engineering.

5. The experimental study and results described below demonstrate that claims 103-110 are supported by a substantial utility. The study was performed using the protocols described in the above-captioned application.

6. A recombinant *Aspergillus oryzae* strain containing a *Thermomyces lanuginosus* lipase gene (Le-1) and a yield- and morphologically improved mutant (7-1) of Le-1 were analyzed using microarrays containing the *Aspergillus oryzae* ESTs disclosed in the above-captioned application. When Le-1 is grown in laboratory fermentors it displays a very pronounced "ballooning" phenotype where the mycelium becomes bloated and fragmented. After approximately 90 hours of fermentation the culture undergoes a significant morphological change and becomes more viscous. Concomitantly the dissolved air tension drops rapidly and production of the lipase ceases. Mutant 7-1 was isolated as a classical mutant of Le-1 by mutagenesis and high-throughput screening. This mutant displays a much lower degree of ballooning and does not display the catastrophic changes in fermentation morphology and productivity. The initial productivity of 7-1 is similar to that of Le-1, but, in contrast to Le-1, does not stop producing lipase after 90 hours.

7. Samples of mRNA extracted from strains Le-1 and 7-1 cultivated in 1 L fermentors for 3 or 4 days were labeled and hybridized to a microarray containing the *Aspergillus oryzae* ESTs described in Appendix A. Each strain was fermented twice yielding a total of 4 samples per strain for microarray analysis. In each hybridization mRNAs from Le-1 and 7-1 were labeled with different fluorophores, mixed, and hybridized to the slide. Samples from Le-1 (day 3) were compared to samples from 7-1 (day 3), and samples from the two strains at four days post inoculum were also compared. A total of 5 hybridizations were performed with mRNA extracted from day 3 samples, and 2 hybridizations were performed with mRNA extracted from day 4 samples. The samples from each strain at day 4 were from the same fermentation and thus represent technical replicates rather than biological replicates. Microarray slides from the hybridizations were scanned and the image data analyzed as described in the above-captioned application. The data from each time point were used as replicates for the identification of significantly differentially regulated genes on a 95% confidence level. This yielded a list of differentially regulated genes from each time point (shown in Appendix A).

8. Analysis revealed a number of genes whose transcript levels differed between the strains. Among these genes were 53 ribosomal genes and 27 genes identified as being involved in cell wall synthesis and morphogenesis, indicating that general protein production and the cell wall metabolism is regulated differently in the strains. These results fit well with the observation that the morphology of the two strains is different, especially with regard to the degree of "ballooning" when expressing the lipase gene.

9. From the list in Appendix A, it is obvious that the ribosomal genes are differentially expressed between the two strains. The 53 ribosomal genes are consistently down-regulated in 7-1 compared to Le-1 on both day 3 and day 4. Similarly, three genes with homology to the translation initiation factor 3 from *Schizosaccharomyces pombe* are down-regulated in 7-1 while 5 of 6 genes with homology to tRNAs are up-regulated in 7-1. The consistent down-regulation of genes involved in translation indicates that 7-1 has generally reduced translational activity compared to Le-1, which may relieve some of the secretional stress and reduce the degree of ballooning seen in Le-1. It may also reduce the counter-selective pressure against lipase-producing cells that may be responsible for the rapid loss of expression potential in Le-1.

cultures after 90 hours of fermentation, allowing 7-1 to retain its expression potential throughout the fermentation. Another explanation could be that the growth rate of the 7-1 cells are lower than that of Le-1. The cultures are dosed approximately the same amount of glucose during fermentation, but the Le-1 culture changes composition rather abruptly in the period leading up to the 90 hours time point. The Le-1 cells that produce lipase become inactive and ultimately die while the culture is taken over by cells that have lost lipase production capacity.

10. The list of differentially regulated genes in Appendix A shows 27 genes involved in cell-wall synthesis. Twenty of these genes are consistently up-regulated while seven are down-regulated in 7-1 compared to Le-1. Figure 1 shows a model for the synthesis of β -glucans in the cell wall of fungi. Some of the genes listed in Appendix A can be assigned (by homology to genes of known or putative function) to the first three steps of cell wall synthesis as depicted in Figure 1. Among the genes that can be assigned to the first step, biosynthesis of linear 1,3- β -glucans, is a homolog of FSK (*Aspergillus fumigatus*, Kelly *et al.* 1996, *J. Bact.* 178: 4381-4391; Beauvais *et al.* 2001, *J. Bact.* 183: 2273-2279), RHO2 (regulator of α -glucan biosynthesis in *S. pombe*, Hirata *et al.* 1998, *J. Cell Sci.* 111: 149-159), RHO-GTPase (same family of proteins as RHO2), and RHO GDP dissociation inhibitor (Sasaki & Takai, 1998, *J. Bact.* 183: 2273-2279). FSK and RHO2 are up-regulated while the RHO GDP dissociation inhibitor is down-regulated. The results suggest that the β -glucan synthesis pathway is up-regulated.

11. Two of the differentially regulated genes in Appendix A can be assigned to the second step in the biosynthesis of β -glucan, namely a protein with homology to a *Fusarium venenatum* glucanase and a protein with homology to an *Aspergillus fumigatus* β -1,3-glucanolsyltransferase. Both proteins have homology to the Bgl2 protein from *Saccharomyces cerevisiae*. The *Aspergillus fumigatus* homolog have been shown to introduce intrachain 1,6- β -linkages into 1,3- β -glucan, although the role of the *Aspergillus fumigatus* protein in cell wall synthesis is yet unclear (Mouyna *et al.*, 1998, *Microbiology* 144: 3171-3180).

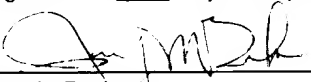
12. Five genes from Appendix A can be assigned to the third step in the pathway shown in Figure 1. Each of these genes has homology to one of the three GEL genes identified in *Aspergillus fumigatus* (Mouyna *et al.*, 2000, *J. Biol. Chem.* 275: 14882-14889; Mouyna *et al.*, 2000, *Biochem. J.* 347: 741-747). The GEL1p protein is the most intensively studied enzyme of the three and encodes a glycosylphosphatidylinositol-anchored β -1,3-glucanolsyltransferase that cleaves a β -1,3-glucan internally and transfers the reducing end to the non-reducing end of another β -1,3-glucan molecule, resulting in elongation of this glucan chain. While deletion of the GEL1p protein does not confer a phenotype to *Aspergillus fumigatus*, a GEL2p mutant has a reduced growth rate and altered conidiation. The GEL3p protein is not expressed in standard culture conditions (Bernard and Latgé, 2001, *Med. Mycol.* 39, suppl. 1, 9-17). In strain 7-1 the GEL1p and GEL2p homologues are up-regulated, but the GEL3p homologues are down-regulated. The regulation patterns of the differentially expressed genes involved in cell-wall synthesis suggest that the β -glucan synthesis pathway is up-regulated in strain 7-1 compared to Le-1. The physiological effect of the increased activity of this pathway is consistent with the reduced ballooning seen in 7-1, since it may be that the ballooning phenotype could be caused by a deficiency of cell-wall components at the hyphae elongation sites, and that this deficiency could be an effect of immense overloading of the secretion machinery in the cells. While the up-regulation of proteins that take part in cell-wall synthesis *in situ* does not reduce the pressure on the secretion pathway, it may increase the secretion of cell-wall synthesis enzymes at the expense of other, less crucial, enzymes.

12. The results described above clearly demonstrate that the microarrays produced from the

Aspergillus oryzae ESTs provide a powerful tool to study the effect of strain differences on global gene expression in the cells. Especially in the context of mutants produced by "classical" means (*i.e.*, by radiation or chemical mutagenesis) the microarray analysis provides one of the very few methods for identifying the genetic targets of the mutagens. Without this technique it would be an almost impossible task to identify the pathways and ideally the genes that are affected by the introduced mutations.

13. The undersigned declarant declares further that all statements made herein of her own knowledge are true and that all statements made on information and belief are believed to be true and further that these statements are made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize any patent issuing thereon.

Signed this 16 day of September 2003



Randy Berka

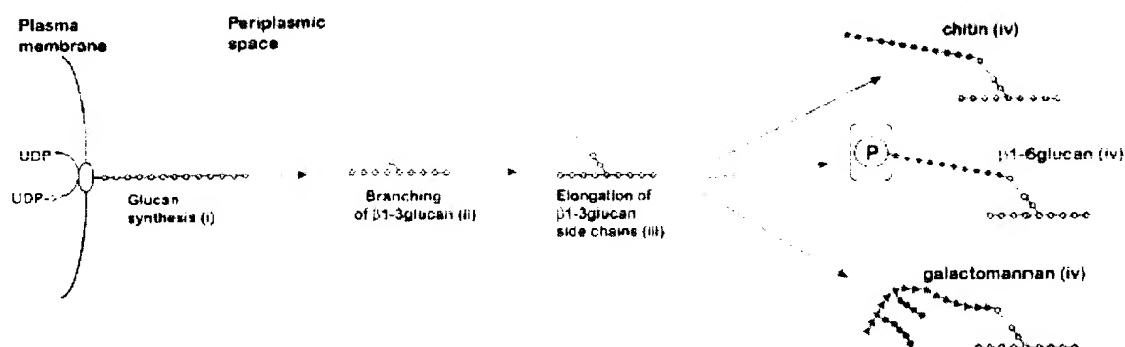


Figure 1. Chronological events involved in the synthesis and postsynthetic modifications of the cell wall 1,3-β-glucans. (i) Biosynthesis of linear 1,3-β-glucan; (ii) branching of 1,3-β-glucans through 1,6-β-glucan side chains; (iii) elongation of 1,3-β-glucan side chains; and (iv) cross-linking of other polymers (chitin and galactomannan in *A. fumigatus*, or chitin, 1,6-β-glucan, and proteins in *S. cerevisiae*) onto non-reducing ends of 1,3-β-glucan side chains. P, proteins. From Mouyna *et al.* 2000a.

Appendix A

Differentially expressed genes in 7-1 compared to Le-1 on day 3 and day 4.

Annotation	Pathway	Fold reg. day 3	Fold reg. day 4
TREMBL:Q9P380 Schizosaccharomyces pombe PUTATIVE PEPTIDE TRANSPORTER.	AA-transport	2,8	2,6
SWISSPROT:P19145 Saccharomyces cerevisiae General amino-acid permease GAP1.	AA-transport	2,6	3,4
SWISSPROT:P53388 Saccharomyces cerevisiae Dicarboxylic amino acid permease.	AA-transport	2,5	3,1
SWISSPROT:P53090 Saccharomyces cerevisiae Aromatic amino acid aminotransferase I (EC 2.6.1.-).	AA-transport	1,4	2,1
SWISSPROT:P38090 Saccharomyces cerevisiae General amino acid permease AGP2.	AA-transport	1,3	1,8
TREMBL:Q96W94 Saccharomyces kluyveri (EC=3.5.1.6) BETA-ALANINE SYNTHASE (EC 3.5.1.6).	AA-metabolism	3,6	2,2
SWISSPROT:Q92413 Emericella nidulans (EC=2.6.1.13) Ornithine aminotransferase (EC 2.6.1.13) (Ornithine-oxo-aci	AA-metabolism	2,1	3,1
TREMBL:Q96V52 Emericella nidulans (EC=6.3.1.2) GLUTAMINE SYNTHETASE (EC 6.3.1.2).	AA-metabolism	1,9	2,4
TREMBL:Q93H39 Streptomyces avermitilis NON-RIBOSOMAL PEPTIDE SYNTHETASE.	AA-metabolism	1,7	1,2
TREMBL:Q9Y7G4 Emericella nidulans CARNITINE/ACYL CARNITINE CARRIER.	AA-metabolism	1,6	1,5
TREMBL:Q9P8T7 Paracoccidioides brasiliensis ORNITHINE DECARBOXYLASE.	AA-metabolism	1,5	1,3
SWISSPROT:Q12611 Emericella nidulans (EC=3.5.3.1) Arginase (EC 3.5.3.1).	AA-metabolism	1,4	1,5
TREMBL:Q9Y7B2 Emericella nidulans (EC=5.4.99.5) CHORISMATE MUTASE (EC 5.4.99.5).	AA-metabolism	1,4	1,4
SWISSPROT:O74787 Schizosaccharomyces pombe (EC=2.1.1.17) Phosphatidylethanolamine N-methyltransferase (EC 2.1.1.17) (AA-metabolism	1,4	1,4
TREMBL:O42652 Schizosaccharomyces pombe (EC=2.6.1.1) PUTATIVE ASPARTATE AMINOTRANSFERASE, CYTOPLASMIC (EC 2.6.1.1	AA-metabolism	-1,3	-3,1
SWISSPROT:P17324 Saccharomyces cerevisiae (EC=4.2.1.13) L-serine dehydratase (EC 4.2.1.13) (L-serine deaminase).	AA-metabolism	-1,5	-10,7
TREMBL:Q9HFU6 Emericella nidulans ORNITHINE DECARBOXYLASE ANTIZYME.	AA-metabolism	-1,6	-2,1
TREMBL:Q96WX7 Emericella nidulans (EC=1.5.1.2) PUTATIVE PYRROLINE-5-CARBOXYLATE REDUCTASE (EC 1.5.1.2).	AA-metabolism	-1,7	-1,6
TREMBL:Q9P444 Emericella nidulans (EC=2.1.1.14) COBALAMIN-INDEPENDENT METHIONINE SYNTHASE (EC 2.1.1.14).	AA-metabolism	-1,8	-1,8
TREMBL:Q9Y7N4 Schizosaccharomyces pombe (EC=1.4.3.3) PUTATIVE D-AMINO ACID OXIDASE (EC 1.4.3.3) (DAMOX) (DAO) (DA	AA-metabolism	-1,9	-1,3
TREMBL:Q8X0I9 Neurospora crassa KETOL-ACID REDUCTOISOMERASE (ILV-2).	AA-metabolism	-2,4	-1,9
SWISSPROT:P38088 Saccharomyces cerevisiae (EC=6.1.1.14) Glycyl-tRNA synthetase (EC 6.1.1.14) (Glycine-tRNA ligase)	tRNA	1,9	1,4
SWISSPROT:P09880 Saccharomyces cerevisiae (EC=6.5.1.3) tRNA ligase (EC 6.5.1.3).	tRNA	1,7	1,4
SWISSPROT:O42870 Schizosaccharomyces pombe (EC=6.1.1.20) Phenylalanyl-tRNA synthetase alpha chain (EC 6.1.1.20) (Phen	tRNA	1,5	1,4
TREMBL:CAD37006 Neurospora crassa Probable tma splicing protein spl1.	tRNA	1,5	1,5
TREMBL:O74781 Schizosaccharomyces pombe (EC=6.1.1.19) PUTATIVE ARGINYL-TRNA SYNTHETASE, CYTOPLASMIC (EC 6.1.1.19)	tRNA	1,4	1,6
SWISSPROT:P04802 Saccharomyces cerevisiae (EC=6.1.1.12) Aspartyl-tRNA synthetase, cytoplasmic (EC 6.1.1.12) (Asparta	tRNA	-1,5	-1,2
SWISSPROT:Q12207 Saccharomyces cerevisiae Non-classical export protein 2.	Transport	-3,6	-4,4
SWISSPROT:O14164 Schizosaccharomyces pombe Probable eukaryotic translation initiation factor 3 93 kDa s	translation	-1,3	-1,3
SWISSPROT:O59742 Schizosaccharomyces pombe Probable eukaryotic translation initiation factor 3 135 kDa	translation	-1,6	-1,8
SWISSPROT:O59742 Schizosaccharomyces pombe Probable eukaryotic translation initiation factor 3 135 kDa	translation	-2,2	-1,4
SWISSPROT:Q9UST4 Schizosaccharomyces pombe Initiation factor 5A-2 (eIF-5A 2).	Transcription	2,3	1,4
TREMBL:Q9P3D9 Neurospora crassa RELATED TO GTP-BINDING PROTEIN RAB2.	Transcription	2,3	2,0
SWISSPROT:Q12753 Saccharomyces cerevisiae Transcriptional activator HAA1.	Transcription	1,7	1,2
TREMBL:Q9HEX7 Pneumocystis carinii HELIX-LOOP-HELIX DNA BINDING PROTEIN	Transcription	1,5	1,4
TREMBL:AAM22470 Fusarium solani Cutinase transcription factor 1 alpha	Transcription	1,4	1,3
SWISSPROT:Q12731 Emericella nidulans Transcription initiation factor TFIID (TATA-box factor) (TAT	Transcription	1,3	1,6
SWISSPROT:P08153 Saccharomyces cerevisiae Transcriptional factor SWI5.	Transcription	1,3	2,4
TREMBL:O59849 Aspergillus oryzae HAPE.	Transcription	1,3	1,5
TREMBL:Q00069 Ascobolus immersus ZINC FINGER PROTEIN.	Transcription	-1,2	-2,4
SWISSPROT:P49373 Schizosaccharomyces pombe Transcription elongation factor S-II (TFIIS).	Transcription	-1,3	-1,3
SWISSPROT:Q92371 Schizosaccharomyces pombe Transcription factor BTF3 homolog.	Transcription	-1,4	-1,3
SWISSPROT:P47943 Schizosaccharomyces pombe Eukaryotic initiation factor 4A (eIF-4A) (eIF4A).	Transcription	-2,1	-1,4
SWISSPROT:Q92794 Homo sapiens Monocytic leukemia zinc finger protein (Zinc finger protein	Transcription	-2,2	-5,5

Annotation	Pathway	Fold reg day 3	Fold reg day 4
GENESEQP:AAE06000 Unidentified Zinc finger protein (ZFP) m1 protein.	Transcription	-2,6	-23,0
TREMBL:Q96WT5 <i>Aspergillus oryzae</i> MALTOSE PERMEASE.	sugar-transport	3,6	6,3
ERDBP:NP000895 <i>Fusarium oxysporum</i> F. oxysporum Glucose Transporter	sugar-transport	1,9	9,5
SWISSPROT:P15325 <i>Emmericella nidulans</i> Quinate permease (Quinate transporter).	sugar-transport	1,8	1,5
TREMBL:Q9P3B9 <i>Neurospora crassa</i> RELATED TO MYO-INOSITOL TRANSPORT PROTEIN ITR1.	sugar-transport	-1,2	-1,9
SWISSPROT:Q92253 <i>Neurospora crassa</i> Probable glucose transporter rco-3	sugar-transport	-2,0	-3,9
SWISSPROT:Q92253 <i>Neurospora crassa</i> Probable glucose transporter rco-3.	sugar-transport	-6,2	-5,1
SWISSPROT:Q9USI5 <i>Schizosaccharomyces pombe</i> Heat shock protein sti1 homolog.	Stress	1,8	2,4
SWISSPROT:P23724 <i>Saccharomyces cerevisiae</i> (EC=3.4.25.1) Potential proteasome component C5 (EC 3.4.25.1) (Multicataly	Stress	1,6	1,6
TREMBL:Q8X041 <i>Neurospora crassa</i> RELATED TO HSP90 ASSOCIATED CO-CHAPERONE.	Stress	1,6	2,4
TREMBL:Q9HGT8 <i>Coccidioides immitis</i> UBIQUITIN CARBOXYL-TERMINAL HYDROLASE (FRAGMENT)	stress	1,4	2,3
SWISSPROT:O74225 <i>Neurospora crassa</i> Heat shock protein Hsp88.	stress	1,3	1,7
TREMBL:Q9P5S4 <i>Neurospora crassa</i> RELATED TO HSP70 PROTEIN	stress	1,3	2,6
SWISSPROT:O74225 <i>Neurospora crassa</i> Heat shock protein Hsp88.	stress	-1,4	-1,5
GENESEQP:AAR43654 <i>Aspergillus nidulans</i> c424 gene product.	Stress	-2,3	-3,7
GENESEQP:AAR43654 <i>Aspergillus nidulans</i> c424 gene product.	Stress	-2,9	-2,8
SWISSPROT:P18899 <i>Saccharomyces cerevisiae</i> DDR48 stress protein (DNA damage-responsive protein 48) (DDR	Stress	-3,0	-3,5
TREMBL:Q9HG46 <i>Aspergillus oryzae</i> PUTATIVE 3-KETOACYL-COA THIOLASE.	Sterol/Lipid met	1,4	1,2
TREMBL:Q29517 <i>Oryctolagus cuniculus</i> (EC=3.1.4.11) PHOSPHOLIPASE C (EC 3.1.4.11) (FRAGMENT)	Sterol/Lipid met	-1,2	-2,1
GENESEQP:AAB19184 <i>Saccharomyces cerevisiae</i> Lipid metabolism protein encoded by the open reading frame Y	Sterol/Lipid met	-1,4	-1,3
SWISSPROT:O59933 <i>Candida albicans</i> C-4 methyl sterol oxidase (EC 1. - - -)	Sterol/Lipid met	-1,6	-6,2
SWISSPROT:O14340 <i>Schizosaccharomyces pombe</i> Oxysterol-binding protein homolog C2F12.05c.	Sterol/Lipid met	-1,8	-3,2
TREMBL:Q9P8R0 <i>Aspergillus fumigatus</i> CYTOCHROME P450 STEROL 14 ALPHA-DEMETHYLASE (14-ALPHA STEROL	Sterol/Lipid met	-2,3	-45,4
TREMBL:Q9P3J7 <i>Neurospora crassa</i> RELATED TO SPORE COAT PROTEIN SP96.	Sporulering	-1,4	-1,2
TREMBL:Q9P3J7 <i>Neurospora crassa</i> RELATED TO SPORE COAT PROTEIN SP96	Sporulering	-2,2	-1,9
TREMBL:Q96UP0 <i>Neurospora crassa</i> PHEROMONE PPG-1-LIKE PROTEIN (PHEROMONE PRECURSOR)	signalling	4,1	20,3
TREMBL:Q9GYW6 <i>Drosophila melanogaster</i> THYROID HORMONE RECEPTOR-ASSOCIATED PROTEIN TRAP170 (FRAGMEN	signalling	1,6	1,5
TREMBL:O74749 <i>Schizosaccharomyces pombe</i> SIMILARITY TO MAMMALIAN SIGNAL TRANSDUCING ADAPTOR	signalling	-1,9	-2,6
TREMBL:Q9JLE9 <i>Rattus norvegicus</i> GABA-A RECEPTOR EPSILON-LIKE SUBUNIT.	signalling	-2,8	-35,8
SWISSPROT:Q04491 <i>Saccharomyces cerevisiae</i> Protein transport protein SEC13.	secretion	1,7	1,9
ERDBP:NP000597 <i>Fusarium venenatum</i> F. venenatum GDI homolog	secretion	1,4	1,6
TREMBL:Q8X0K7 <i>Neurospora crassa</i> RELATED TO SECRETORY PROTEIN SSP120.	secretion	-1,3	-3,1
SWISSPROT:P53619 <i>Bos taurus</i> Coatomer delta subunit (Delta-coat protein) (Delta-COP).	secretion	-1,6	-1,5
TREMBL:Q8X079 <i>Neurospora crassa</i> RELATED TO RNA HELICASE/RNASEIII CAF.	RNA	1,7	1,3
TREMBL:O00870 <i>Trypanosoma brucei</i> RIBONUCLEASE H1.	RNA	1,6	1,2
TREMBL:Q9CWZ3 <i>Mus musculus</i> 2310057C03RIK PROTEIN (RNA BINDING MOTIF PROTEIN 8A)	RNA	1,3	2,1
SWISSPROT:Q07478 <i>Saccharomyces cerevisiae</i> Probable ATP-dependent RNA helicase SUB2.	RNA	1,3	1,7
TREMBL:Q9Y7A8 <i>Neurospora crassa</i> PAD-1.	RNA	1,3	1,9
TREMBL:Q9P3U1 <i>Schizosaccharomyces pombe</i> PROTEIN WITH 3 RNA BINDING DOMAINS, YEAST HRB1 HOMOLOGUE	RNA	-1,3	-1,4
TREMBL:Q9P3E1 <i>Neurospora crassa</i> RELATED TO RNA-BINDING PROTEIN FUS/TLS.	RNA	-1,3	-1,7
TREMBL:Q9UQ35 <i>Homo sapiens</i> RNA BINDING PROTEIN	RNA	-1,8	-1,3
SWISSPROT:O74330 <i>Schizosaccharomyces pombe</i> 40S ribosomal protein S27	Ribosomal	-1,2	-1,6
SWISSPROT:P53163 <i>Saccharomyces cerevisiae</i> Putative 60S ribosomal protein L7/L12 homolog, mitochondrial	Ribosomal	-1,2	-1,7
SWISSPROT:P23369 <i>Saccharomyces cerevisiae</i> Mitochondrial 60S ribosomal protein L25 (Yml 25)	Ribosomal	-1,3	-1,4
SWISSPROT:Q10157 <i>Schizosaccharomyces pombe</i> 60S ribosomal protein L11.	Ribosomal	-1,4	-1,4
SWISSPROT:O42952 <i>Schizosaccharomyces pombe</i> 40S ribosomal protein S30.	Ribosomal	-1,4	-1,4
SWISSPROT:P49631 <i>Saccharomyces cerevisiae</i> 60S ribosomal protein L43 (L37A) (Yl 35)	Ribosomal	-1,4	-1,7
SWISSPROT:Q9P3T6 <i>Schizosaccharomyces pombe</i> 40S ribosomal protein S5-B.	Ribosomal	-1,4	-1,5
SWISSPROT:O74836 <i>Schizosaccharomyces pombe</i> 60S ribosomal protein L1-B (L10a)	Ribosomal	-1,5	-2,6

Annotation	Pathway	Fold reg day 3	Fold reg day 4
SWISSPROT:Q9C0T1 <i>Emmericella nidulans</i> 60S ribosomal protein L37.	Ribosomal	-1,5	-1,3
SWISSPROT:O60128 <i>Schizosaccharomyces pombe</i> 40S ribosomal protein S3.	Ribosomal	-1,5	-1,6
SWISSPROT:O74172 <i>Schizosaccharomyces pombe</i> 40S ribosomal protein S25-B (S31-B).	Ribosomal	-1,5	-2,0
SWISSPROT:O59953 <i>Neurospora crassa</i> 60S ribosomal protein L5 (CPR4).	Ribosomal	-1,6	-1,4
SWISSPROT:P34737 <i>Podospora anserina</i> 40S ribosomal protein S15 (S12).	Ribosomal	-1,6	-1,5
SWISSPROT:Q9HFR7 <i>Trichoderma hamatum</i> 60S ribosomal protein L36 (TRP36).	Ribosomal	-1,6	-1,3
SWISSPROT:P78987 <i>Erysiphe graminis</i> 60S ribosomal protein L27A (L29).	Ribosomal	-1,6	-1,5
SWISSPROT:P26781 <i>Saccharomyces cerevisiae</i> 40S ribosomal protein S11 (S18) (YS12) (RP41).	Ribosomal	-1,7	-1,7
SWISSPROT:O13672 <i>Schizosaccharomyces pombe</i> 60S ribosomal protein L8 (L7A) (L4).	Ribosomal	-1,7	-1,7
TREMBL:Q9P4Z0 <i>Neurospora crassa</i> PROBABLE RIBOSOMAL PROTEIN RPS8BP	Ribosomal	-1,7	-1,3
SWISSPROT:Q9HE25 <i>Neurospora crassa</i> 60S ribosomal protein L17.	Ribosomal	-1,7	-1,8
SWISSPROT:Q9USX4 <i>Schizosaccharomyces pombe</i> 60S ribosomal protein L33-A (L37A).	Ribosomal	-1,7	-1,6
SWISSPROT:P21772 <i>Neurospora crassa</i> 40S ribosomal protein S26E (CRP5) (13.6 kDa ribosomal protein)	Ribosomal	-1,8	-1,4
TREMBL:Q9C2B9 <i>Neurospora crassa</i> PROBABLE RIBOSOMAL PROTEIN L38.	Ribosomal	-1,8	-1,9
SWISSPROT:P04451 <i>Saccharomyces cerevisiae</i> 60S ribosomal protein L23 (L17).	Ribosomal	-1,8	-1,3
SWISSPROT:O13418 <i>Aspergillus niger</i> 60S ribosomal protein L15.	Ribosomal	-1,8	-1,8
TREMBL:Q9C2H7 <i>Neurospora crassa</i> PROBABLE RIBOSOMAL PROTEIN RPL4A.	Ribosomal	-1,8	-1,5
SWISSPROT:P21772 <i>Neurospora crassa</i> 40S ribosomal protein S26E (CRP5) (13.6 kDa ribosomal protein)	Ribosomal	-1,9	-1,5
SWISSPROT:P79015 <i>Schizosaccharomyces pombe</i> 60S ribosomal protein L32-A.	Ribosomal	-1,9	-2,0
SWISSPROT:Q9P7B2 <i>Schizosaccharomyces pombe</i> 40S ribosomal protein S8-B.	Ribosomal	-1,9	-1,7
TREMBL:Q9HGV0 <i>Aspergillus fumigatus</i> ACIDIC RIBOSOMAL PROTEIN P1.	Ribosomal	-2,0	-1,4
TREMBL:Q96W54 <i>Candida albicans</i> RIBOSOMAL PROTEIN S22.	Ribosomal	-2,0	-1,8
SWISSPROT:P05736 <i>Saccharomyces cerevisiae</i> 60S ribosomal protein L2 (YL6) (L5) (RP8).	Ribosomal	-2,1	-1,2
TREMBL:Q9USW5 <i>Schizosaccharomyces pombe</i> 40S RIBOSOMAL PROTEIN S4-2.	Ribosomal	-2,1	-1,3
TREMBL:Q9C2B9 <i>Neurospora crassa</i> PROBABLE RIBOSOMAL PROTEIN L38.	Ribosomal	-2,1	-5,1
SWISSPROT:O60143 <i>Schizosaccharomyces pombe</i> 60S ribosomal protein L7-C.	Ribosomal	-2,1	-1,6
SWISSPROT:Q10421 <i>Schizosaccharomyces pombe</i> 40S ribosomal protein S28 (S33).	Ribosomal	-2,2	-1,6
TREMBL:Q96UT5 <i>Paracoccidioides brasiliensis</i> PUTATIVE RIBOSOMAL PROTEIN L35.	Ribosomal	-2,2	-1,5
TREMBL:Q9C3Z6 <i>Podospora anserina</i> RIBOSOMAL PROTEIN P0.	Ribosomal	-2,2	-1,3
SWISSPROT:P36105 <i>Saccharomyces cerevisiae</i> 60S ribosomal protein L14-A.	Ribosomal	-2,2	-1,5
SWISSPROT:P52810 <i>Podospora anserina</i> 40S ribosomal protein S9 (S7).	Ribosomal	-2,2	-1,6
TREMBL:Q9URK4 <i>Schizosaccharomyces pombe</i> RIBOSOMAL PROTEIN S16 HOMOLOG (FRAGMENT).	Ribosomal	-2,3	-1,3
TREMBL:Q9HDQ7 <i>Colletotrichum gloeosporioides</i> PUTATIVE 60S RIBOSOMAL PROTEIN	Ribosomal	-2,3	-1,9
SWISSPROT:O59953 <i>Neurospora crassa</i> 60S ribosomal protein L5 (CPR4).	Ribosomal	-2,3	-1,5
TREMBL:CAD37159 <i>Aspergillus fumigatus</i> Putative ribosomal protein.	Ribosomal	-2,3	-1,3
SWISSPROT:O14069 <i>Schizosaccharomyces pombe</i> Probable 60S ribosomal protein C1687 06c	Ribosomal	-2,4	-1,3
TREMBL:AAM43909 <i>Aspergillus fumigatus</i> Large subunit ribosomal protein L3.	Ribosomal	-2,4	-1,5
TREMBL:CAA37766 <i>Neurospora crassa</i> Ribosomal protein crp-2	Ribosomal	-2,4	-2,1
SWISSPROT:Q09668 <i>Schizosaccharomyces pombe</i> 60S ribosomal protein L22.	Ribosomal	-2,4	-2,2
TREMBL:Q96W42 <i>Ophiostoma novo-ulmi</i> RIBOSOMAL PROTEIN L34-LIKE PROTEIN.	Ribosomal	-2,4	-2,0
SWISSPROT:P27073 <i>Emmericella nidulans</i> 40S ribosomal protein S19 (S16).	Ribosomal	-2,4	-1,9
SWISSPROT:O74892 <i>Schizosaccharomyces pombe</i> 40S ribosomal protein S2.	Ribosomal	-2,6	-1,2
TREMBL:Q9UVN8 <i>Emmericella nidulans</i> RIBOSOMAL PROTEIN L16A	Ribosomal	-2,7	-1,5
SWISSPROT:Q10192 <i>Schizosaccharomyces pombe</i> 60S ribosomal protein L18	Ribosomal	-2,7	-1,4
SWISSPROT:O74893 <i>Schizosaccharomyces pombe</i> 40S ribosomal protein S20.	Ribosomal	-2,7	-1,6
SWISSPROT:Q9C0Z7 <i>Schizosaccharomyces pombe</i> 40S ribosomal protein S6-B.	Ribosomal	-2,7	-1,4
TREMBL:Q9HFB3 <i>Aspergillus oryzae</i> PACC.	reguleng	2,4	1,3
TREMBL:Q9UVK6 <i>Emmericella nidulans</i> MITOGEN-ACTIVATED PROTEIN KINASE.	reguleng	2,1	1,3
TREMBL:Q9HET3 <i>Aspergillus niger</i> SECRETION RELATED GTPASE (SRGB)	reguleng	1,8	2,2
TREMBL:Q9Y899 <i>Emmericella nidulans</i> CALCIUM/CALMODULIN DEPENDENT PROTEIN KINASE B.	reguleng	1,7	1,3
TREMBL:Q9P5Z9 <i>Neurospora crassa</i> RELATED TO NIF-SPECIFIC REGULATORY PROTEIN.	reguleng	1,5	1,7
SWISSPROT:P36586 <i>Schizosaccharomyces pombe</i> Ras-related protein ypt5.	reguleng	1,5	1,4

Annotation	Pathway	Fold reg. day 3	Fold reg. day 4
TREMBL:O74251 <i>Emicella nidulans</i> MEDUSA.	regulating	1,4	1,9
SWISSPROT:P87072 <i>Neurospora crassa</i> Calcineurin B subunit (Protein phosphatase 2B regulatory sub	regulating	1,4	1,9
TREMBL:Q8WZR7 <i>Neurospora crassa</i> PROBABLE GTP-BINDING PROTEIN DRAB11.	regulating	1,3	1,9
TREMBL:Q9C297 <i>Neurospora crassa</i> RAS-2 PROTEIN.	regulating	-1,3	-1,9
SWISSPROT:Q00771 <i>Emicella nidulans</i> (EC=2.7.1.123) Calcium/calmodulin-dependent protein kinase (EC 2.7.1.123) (Regulating	-2,2	-1,3
TREMBL:Q10294 <i>Schizosaccharomyces pombe</i> CAMP-INDEPENDENT REGULATORY PROTEIN PAC2.	Regulating	-3,4	-8,4
GENESEQ:ABP60744 <i>Aspergillus nidulans</i> <i>Aspergillus nidulans</i> thioredoxin SEQ ID NO:93.	redox	-1,2	-2,1
TREMBL:Q9HFR2 <i>Ajellomyces capsulata</i> PUTATIVE THIOL-SPECIFIC ANTIOXIDANT PROTEIN TSA1.	redox	-1,3	-2,3
TREMBL:Q9P5T9 <i>Neurospora crassa</i> PROBABLE NI-BINDING UREASE ACCESSORY PROTEIN (UREG).	purine/pyrimidine metabolism	1,7	1,5
TREMBL:BAC07276 <i>Neurospora crassa</i> (EC=6.3.2.6) 5'-phosphonobosyl-5-aminoimidazole-4-N-succinocarbonyl s	purine/pyrimidine metabolism	-1,3	-1,6
TREMBL:Q12610 <i>Emicella nidulans</i> (EC=1.3.1.14) DIHYDROOROTATE DEHYDROGENASE (EC 1.3.1.14)	purine/pyrimidine metabolism	-1,4	-1,6
TREMBL:CAD37041 <i>Neurospora crassa</i> Nucleoside-diphosphate kinase	purine/pyrimidine metabolism	-1,7	-2,2
TREMBL:Q9UTG1 <i>Schizosaccharomyces pombe</i> PUTATIVE PURINE NUCLEOSIDE PHOSPHORYLASE.	purine/pyrimidine metabolism	-2,2	-1,6
TREMBL:Q8X175 <i>Emicella nidulans</i> KARYOPHERIN ALPHA	protein transport nucleus	-1,4	-1,4
TREMBL:Q93914 <i>Aspergillus niger</i> PDI RELATED PROTEIN A.	Protein folding	2,9	5,9
TREMBL:Q9C2N6 <i>Neurospora crassa</i> RELATED TO DNAJ-LIKE PROTEIN HOMOLOG.	Protein folding	1,9	1,8
TREMBL:Q9HGM9 <i>Schizosaccharomyces pombe</i> DNAJ DOMAIN PROTEIN SIMILAR TO HUMAN TETRATRICOPEPTIDE REPEA	Protein folding	1,8	1,2
TREMBL:Q8X0V3 <i>Neurospora crassa</i> PROBABLE PEROXISOMAL PROTEIN POX18.	peroxisom	1,6	1,8
TREMBL:Q8WZW4 <i>Neurospora crassa</i> RELATED TO PEROXISOMAL MEMBRANE PROTEIN PMP47B.	peroxisom	-1,7	-2,1
TREMBL:Q59632 <i>Ochrobactrum anthropi</i> (EC=3.4.11.19) D-AMINOPEPTIDASE (EC 3.4.11.19).	peptidase/protease	3,2	5,1
TREMBL:Q96VC4 <i>Emicella nidulans</i> CARBOXYPEPTIDASE.	peptidase/protease	1,9	1,6
TREMBL:Q96VT2 <i>Aspergillus niger</i> (EC=3.4.11.5) PROLYL AMINOPEPTIDASE A (EC 3.4.11.5)	peptidase/protease	1,5	2,4
TREMBL:Q98L22 <i>Rhizobium loti</i> PROLINE DIPEPTIDASE.	peptidase/protease	1,3	2,4
TREMBL:Q9UUR7 <i>Metarhizium anisopliae</i> METALLOPROTEASE MEP1.	peptidase/protease	-1,5	-1,4
TREMBL:AAM55216 <i>Alcaligenes eutrophus</i> 6-chlorohydroxyquinol-1,2-dioxygenase.	Mitochondriel	3,0	1,5
SWISSPROT:P14187 <i>Neurospora crassa</i> (EC=4.4.1.17) Cytochrome c heme lyase (EC 4.4.1.17) (CCHL) (Holocytochrome	Mitochondriel	2,2	1,3
TREMBL:Q8WZY6 <i>Neurospora crassa</i> PROBABLE COPROPORPHYRINOGEN OXIDASE.	Mitochondriel	1,7	1,9
SWISSPROT:P00431 <i>Saccharomyces cerevisiae</i> (EC=1.11.1.5) Cytochrome C peroxidase, mitochondrial precursor (EC 1.11.1.	Mitochondriel	1,4	2,3
SWISSPROT:Q07536 <i>Bos taurus</i> (EC=1.2.1.27) Methylmalonate-semialdehyde dehydrogenase [acylating], mitoc	Mitochondriel	1,4	1,8
TREMBL:Q9Y857 <i>Kluyveromyces lactis</i> (EC=1.1.2.3) CYTOCHROME B2 PRECURSOR (EC 1.1.2.3)	Mitochondriel	1,4	3,7
TREMBL:O74752 <i>Schizosaccharomyces pombe</i> PUTATIVE MITOCHONDRIAL PROTEIN IMPORT PROTEIN.	Mitochondriel	1,3	2,2
SWISSPROT:Q9Y8A7 <i>Emicella nidulans</i> Mitochondrial import inner membrane translocase subunit TIM9	Mitochondriel	-1,2	-1,8
SWISSPROT:P39515 <i>Saccharomyces cerevisiae</i> Mitochondrial import inner membrane translocase subunit TIM1	Mitochondriel	-1,2	-1,7
SWISSPROT:P38364 <i>Fusarium solani</i> Pisatin demethylase (EC 1.14.-.-) (Cytochrome P450 57A2).	Mitochondriel	-1,2	-2,0
SWISSPROT:Q9UUZ9 <i>Aspergillus oryzae</i> Thiazole biosynthetic enzyme, mitochondrial precursor.	Mitochondriel	-1,2	-2,2
TREMBL:P87230 <i>Schizosaccharomyces pombe</i> PUTATIVE UBIQUINONE BIOSYNTHESIS METHYLTRANSFERASE C4G3.04C(Mitochondriel	-1,3	-1,4
TREMBL:Q94EK6 <i>Pisum sativum</i> FERRIC-CHELATE REDUCTASE.	Mitochondriel	-1,3	-1,6
TREMBL:Q8WZW6 <i>Neurospora crassa</i> RELATED TO ATP SYNTHASE EPSILON CHAIN (MITOCHONDRIAL).	Mitochondriel	-1,3	-1,3
SWISSPROT:O74471 <i>Schizosaccharomyces pombe</i> Cytochrome c oxidase polypeptide via. mitochondrial precursor	Mitochondriel	-1,3	-2,1
SWISSPROT:Q12233 <i>Saccharomyces cerevisiae</i> (EC=3.6.3.14) ATP synthase G chain, mitochondrial (EC 3.6.3.14)	Mitochondriel	-1,3	-1,9
TREMBL:BAC10043 <i>Oryza sativa</i> Putative cytochrome P450.	Mitochondriel	-1,3	-1,3
SWISSPROT:O13350 <i>Kluyveromyces lactis</i> (EC=3.6.3.14) ATP synthase D chain, mitochondrial (EC 3.6.3.14).	Mitochondriel	-1,3	-1,5
TREMBL:Q9C1X2 <i>Schizosaccharomyces pombe</i> PUTATIVE D-LACTATE DEHYDROGENASE MITOCHONDRIAL	Mitochondriel	-1,4	-2,6
SWISSPROT:P17505 <i>Saccharomyces cerevisiae</i> (EC=1.1.1.37) Malate dehydrogenase, mitochondrial precursor (EC 1.1.1.37)	Mitochondriel	-1,4	-1,4
SWISSPROT:O74533 <i>Schizosaccharomyces pombe</i> (EC=1.10.2.2) Probable ubiquinol-cytochrome C reductase complex 14 kDa pro	Mitochondriel	-1,4	-1,6

Annotation	Pathway	Fold reg. day 3	Fold reg. day 4
TREMBL:Q93980 <i>Aspergillus niger</i> CYTOCHROME C OXIDASE SUBUNIT V.	Mitochondrial	-1.4	-2.3
SWISSPROT:P00427 <i>Saccharomyces cerevisiae</i> (EC=1.9.3.1) Cytochrome c oxidase polypeptide VI, mitochondrial precursor	Mitochondrial	-1.5	-1.6
TREMBL:Q8WZ88 <i>Neurospora crassa</i> PROBABLE YHM1 (MITOCHONDRIAL CARRIER).	Mitochondrial	-1.5	-1.2
SWISSPROT:P40086 <i>Saccharomyces cerevisiae</i> Cytochrome c oxidase assembly protein COX15.	Mitochondrial	-1.6	-1.5
TREMBL:Q9P5U4 <i>Neurospora crassa</i> GRPE PROTEIN HOMOLOG.	Mitochondrial	-1.6	-2.5
SWISSPROT:P37211 <i>Neurospora crassa</i> (EC=3.6.3.14) ATP synthase alpha chain, mitochondrial precursor (EC 3.6.3.	Mitochondrial	-1.6	-1.3
SWISSPROT:P09940 <i>Pichia jadinii</i> ATPase inhibitor, mitochondrial.	Mitochondrial	-1.7	-2.2
SWISSPROT:Q92328 <i>Saccharomyces cerevisiae</i> Mitochondrial inheritance component MDM12.	Mitochondrial	-1.7	-1.3
SWISSPROT:P81449 <i>Saccharomyces cerevisiae</i> (EC=3.6.3.14) ATP synthase e chain, mitochondrial (EC 3.6.3.14).	Mitochondrial	-1.7	-1.3
TREMBL:Q94284 <i>Schizosaccharomyces pombe</i> SULFIDE:QUINONE OXIDOREDUCTASE PRECURSOR (EC 1.-.-).	Mitochondrial	-1.8	-2.5
SWISSPROT:P56525 <i>Neurospora crassa</i> (EC=3.6.3.14) ATP synthase delta chain, mitochondrial precursor (EC 3.6.3.	Mitochondrial	-1.8	-1.7
SWISSPROT:P56205 <i>Aspergillus niger</i> Cytochrome c.	Mitochondrial	-1.8	-3.1
SWISSPROT:P02723 <i>Neurospora crassa</i> ADP,ATP carrier protein (ADP/ATP translocase) (Adenine nucle	Mitochondrial	-1.8	-1.5
TREMBL:Q94705 <i>Schizosaccharomyces pombe</i> (EC=1.9.3.1) PUTATIVE CYTOCHROME C OXIDASE POLYPEPTIDE C1259 05C (EC 1.9.	Mitochondrial	-2.1	-2.7
ERDBP:NP000634 <i>Aspergillus oryzae</i> Deduced amino acid sequence for A.oryzae EST AO365 having hi	metabolism	3.0	4.8
ERDBP:NP000634 <i>Aspergillus oryzae</i> Deduced amino acid sequence for A.oryzae EST AO365 having hi	metabolism	2.8	4.8
TREMBL:Q97DL0 <i>Clostridium acetobutylicum</i> AMIDASE FROM NICOTINAMIDASE FAMILY.	metabolism	2.6	11.4
TREMBL:P87017 <i>Aspergillus parasiticus</i> SHORT-CHAIN ALCOHOL DEHYDROGENASE.	metabolism	2.3	2.1
SWISSPROT:P07547 <i>Emmericella nidulans</i> (EC=2.5.1.19) Pentafunctional AROM polypeptide [includes: 3-dehydroquinone	metabolism	2.2	3.5
TREMBL:AAM43715 <i>Dictyostelium discoideum</i> Putative Guanine-nucleotide releasing factor.	metabolism	2.1	2.3
TREMBL:Q9HEE3 <i>Neurospora crassa</i> RELATED TO SORBITOL UTILIZATION PROTEIN SOU1.	metabolism	2.0	3.8
TREMBL:Q96V04 <i>Magnaporthe oryzae</i> ACETOLACTATE SYNTHASE SMALL-SUBUNIT-LIKE PROTEIN.	metabolism	2.0	1.2
TREMBL:Q8X1W7 <i>Monascus anka</i> ACID PHOSPHATASE	metabolism	2.0	1.5
TREMBL:Q9X9X1 <i>Streptomyces coelicolor</i> PUTATIVE ZINC-BINDING DEHYDROGENASE.	metabolism	1.7	1.6
SWISSPROT:P16928 <i>Emmericella nidulans</i> (EC=6.2.1.1) Acetyl-coenzyme A synthetase (EC 6.2.1.1) (Acetate--CoA liga	metabolism	1.7	1.7
SWISSPROT:Q01278 <i>Neurospora crassa</i> (EC=3.6.3.14) Vacuolar ATP synthase subunit E (EC 3.6.3.14) (V-ATPase E su	metabolism	1.6	1.2
ERDBP:NP000805 <i>Aspergillus niger</i> hemA (5-aminolevulinic acid synthase) gene of <i>Aspergillus niger</i>	metabolism	1.5	1.3
TREMBL:Q9P3R9 <i>Neurospora crassa</i> PROBABLE NICOTINATE-NUCLEOTIDE PYROPHOSPHORYLASE (CARBOXYLAT	metabolism	1.5	1.4
TREMBL:Q14344 <i>Schizosaccharomyces pombe</i> (EC=1.1.1.205) PROBABLE INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE (EC 1.1.1.20	metabolism	1.5	3.8
SWISSPROT:Q09751 <i>Schizosaccharomyces pombe</i> (EC=4.4.1.5) Probable lactoylglutathione lyase (EC 4.4.1.5) (Methylglyoxa	metabolism	1.5	1.3
TREMBL:Q74624 <i>Trichoderma reesei</i> (EC=2.7.7.13) MANNANOSE-1-PHOSPHATE GUANYLTRANSFERASE (EC 2.7.7.13) (MPG1 TR	metabolism	1.5	1.5
GENESEQP:AA18136 <i>Thielavia terrestris</i> T. terrestris uroporphyrinogen decarboxylase protein sequenc	metabolism	1.4	1.4
GENESEQP:AAM00105 <i>Physcomitrella patens</i> Triosephosphate transporter sequence #173.	metabolism	1.4	2.8
TREMBL:Q12707 <i>Sporobolomyces salmonicolor</i> (EC=1.1.1.2) NADPH-DEPENDENT ALDEHYDE REDUCTASE (EC 1.1.1.2).	metabolism	1.4	1.2
SWISSPROT:Q12657 <i>Penicillium chrysogenum</i> (EC=2.7.1.25) Adenylylsulfate kinase (EC 2.7.1.25) (APS kinase) (Adenosine	metabolism	1.3	1.7
TREMBL:Q9Y7D1 <i>Aspergillus terreus</i> TRANSESTERASE.	metabolism	-1.2	-3.4
TREMBL:Q9AGP8 <i>Arthrobacter globiformis</i> N,N-DIMETHYLGLYCINE OXIDASE.	metabolism	-1.5	-1.7
TREMBL:Q9Z4Y6 <i>Streptomyces coelicolor</i> PUTATIVE SALICYLATE HYDROXYLASE	metabolism	-1.7	-1.9
TREMBL:Q96WL1 <i>Aspergillus parasiticus</i> AFLATOXIN EFFLUX PUMP AFLT	metabolism	-1.7	-1.4
SWISSPROT:P42882 <i>Aspergillus parasiticus</i> NMT1 protein homolog	metabolism	-1.9	-4.5
TREMBL:Q9FC45 <i>Streptomyces coelicolor</i> PUTATIVE INTEGRAL MEMBRANE PROTEIN.	membrane	2.2	4.3
TREMBL:Q9P5Y3 <i>Neurospora crassa</i> RELATED TO SYNTAXIN 8.	membrane	1.8	1.9
TREMBL:Q8X090 <i>Neurospora crassa</i> RELATED TO SYNTAXIN 12.	membrane	1.8	1.6
TREMBL:Q13312 <i>Aspergillus parasiticus</i> SYNAPTOBREVIN	membrane	1.5	1.7
TREMBL:Q9P864 <i>Pichia jadinii</i> PUTATIVE MEMBRANE PROTEIN.	membrane	1.5	1.7
TREMBL:Q8X175 <i>Emmericella nidulans</i> KARYOPHERIN ALPHA.	membrane	1.4	1.3
TREMBL:Q13657 <i>Schizosaccharomyces pombe</i> PROBABLE MEMBRANE PROTEIN YOL130W	membrane	1.4	1.5

Annotation	Pathway	Fold reg day 3	Fold reg day 4
TREMBL Q9UUX8 <i>Neurospora crassa</i> P-TYPE ATPASE (FRAGMENT).	Ion-transport	1,9	2,5
TREMBL Q9HE83 <i>Neurospora crassa</i> PROBABLE PHOSPHATE TRANSPORT PROTEIN MIR1.	Ion-transport	-1,3	-2,5
TREMBL Q96TH7 <i>Aspergillus fumigatus</i> PLASMA MEMBRANE H ⁺ -ATPASE	Ion-transport	-1,4	-1,6
TREMBL O59940 <i>Neurospora crassa</i> CALCIUM/PROTON EXCHANGER.	Ion-transport	-1,4	-4,0
SWISSPROT Q13733 <i>Homo sapiens</i> (EC=3.6.3.9) Sodium/potassium-transporting ATPase alpha-4 chain (EC 3.6.3)	Ion-transport	-1,5	-1,8
TREMBL Q38998 <i>Arabidopsis thaliana</i> AKT1 POTASSIUM TRANSPORTER.	Ion-transport	-1,6	-1,3
TREMBL Q9HE83 <i>Neurospora crassa</i> PROBABLE PHOSPHATE TRANSPORT PROTEIN MIR1.	Ion-transport	-1,8	-2,4
TREMBL Q9P426 <i>Ajellomyces capsulata</i> N-GLYCOSYL-TRANSFERASE.	Glycosylating Golgi	1,9	2,0
TREMBL Q96VV1 <i>Aspergillus awamori</i> PROTEIN O-MANNOSYL TRANSFERASE.	Glycosylating	1,8	1,7
GENESEQP AAR47201 <i>Saccharomyces cerevisiae</i> DPM2 mannosyl transferase.	Glycosylating	-1,9	-2,0
TREMBL AAL82734 <i>Aspergillus fumigatus</i> Structural maintenance of chromosome protein.	DNA	2,2	2,4
TREMBL O14147 <i>Schizosaccharomyces pombe</i> HYPOTHETICAL 96.2 KDA HELICASE C3G6.11 IN CHROMOSOME 1	DNA	1,6	2,4
SWISSPROT Q9P6Q5 <i>Schizosaccharomyces pombe</i> (EC=3.6.1.23) Probable deoxyuridine 5'-triphosphate nucleotidohydrolase (EC	DNA	1,5	1,6
TREMBL Q8X0K1 <i>Neurospora crassa</i> RELATED TO POL12 (DNA-DIRECTED DNA POLYMERASE ALPHA).	DNA	1,5	1,5
TREMBL O94395 <i>Schizosaccharomyces pombe</i> PUTATIVE ATP-DEPENDENT DNA HELICASE.	DNA	1,4	1,8
SWISSPROT Q09176 <i>Schizosaccharomyces pombe</i> Splicing factor U2AF 23 kDa subunit (U2 auxiliary factor 23	DNA	1,4	1,5
SWISSPROT P48003 <i>Schizosaccharomyces pombe</i> Histone H2A variant.	DNA	1,4	1,2
TREMBL Q9P3G2 <i>Neurospora crassa</i> (EC=1.17.4.1) RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE LARGE CHAIN (EC 1.17.4.	DNA	1,3	2,3
TREMBL CAD37005 <i>Neurospora crassa</i> Related to mismatched base pair and cruciform dna recognition	DNA	-2,0	-8,9
SWISSPROT O75001 <i>Schizosaccharomyces pombe</i> DNA replication licensing factor mcm7 (Minichromosome maintenance	DNA	-2,6	-1,9
GENESEQP AAU00959 <i>Fusarium venenatum</i> F. venenatum glucanase polypeptide.	Cell-wall	5,9	4,6
TREMBL Q9P8U4 <i>Aspergillus fumigatus</i> BETA (1-3) GLUCANOSYLTRANSFERASE GEL2P.	Cell-wall	2,2	2,7
SWISSPROT Q09196 <i>Schizosaccharomyces pombe</i> Myosin regulatory light chain cdc4.	cell-wall	1,9	1,9
TREMBL Q9HFQ2 <i>Emmericella nidulans</i> (EC=3.1.3.16) PROTEIN PHOSPHATASE 2A.	Cell-wall	1,9	1,5
TREMBL Q96UK5 <i>Coccidioides immitis</i> BETA-GLUCOSIDASE 5 (FRAGMENT).	Cell-wall	1,9	1,3
TREMBL Q9P8U4 <i>Aspergillus fumigatus</i> BETA (1-3) GLUCANOSYLTRANSFERASE GEL2P.	Cell-wall	1,8	2,2
TREMBL Q52423 <i>Pseudomonas</i> sp. ENDO ALPHA-1,4 POLYGALACTOSAMINIDASE PRECURSOR.	Cell-wall	1,7	3,8
TREMBL O74687 <i>Aspergillus fumigatus</i> GEL1 PROTEIN.	Cell-wall	1,7	1,6
TREMBL Q8WZQ2 <i>Neurospora crassa</i> RELATED TO CEL1 PROTEIN.	Cell-wall	1,7	24,2
SWISSPROT P40414 <i>Saccharomyces cerevisiae</i> Tropomyosin 2.	cell-wall	1,7	1,3
TREMBL Q92225 <i>Emmericella nidulans</i> 1,3-BETA-D-GLUCAN SYNTHASE CATALYTIC SUBUNIT.	Cell-wall	1,7	1,2
TREMBL Q9C1M3 <i>Emmericella nidulans</i> SEPTIN.	cell-wall	1,5	2,3
TREMBL Q9C1M3 <i>Emmericella nidulans</i> SEPTIN.	cell-wall	1,5	1,6
SWISSPROT Q10133 <i>Schizosaccharomyces pombe</i> Rho2 protein.	Cell-Wall	1,5	2,1
TREMBL Q9UR09 <i>Schizosaccharomyces pombe</i> CELL WALL SYNTHESIS PROTEIN PSU1	cell-wall	1,5	2,0
TREMBL AAN00330 <i>Streptococcus agalactiae</i> Cell wall surface anchor family protein	cell-wall	1,4	1,6
TREMBL Q9P7E8 <i>Schizosaccharomyces pombe</i> ACTIN BINDING PROTEIN WITH SH3 DOMAINS.	Cell-Wall	1,4	1,6
TREMBL Q9C1M2 <i>Emmericella nidulans</i> SEPTIN.	cell-wall	1,4	1,5
TREMBL Q96VD0 <i>Xanthoria parietina</i> HYDROPHOBIN H1 PRECURSOR.	cell-wall	1,3	1,5
TREMBL Q9C3Y4 <i>Emmericella nidulans</i> RHO GTPASE.	Cell-Wall	1,3	1,5
TREMBL Q9P302 <i>Emmericella nidulans</i> HYPERCELLULAR PROTEIN.	Cell-Wall	-1,4	-1,3
TREMBL Q9C1L5 <i>Neurospora crassa</i> PUTATIVE RHO GDP DISSOCIATION INHIBITOR G6G8 3	Cell-Wall	-1,4	-1,3
TREMBL CAD22154 <i>Volvox carter</i> Pherophorin-dz1 protein.	Cell-Wall	-1,7	-4,6
TREMBL Q9P8U3 <i>Aspergillus fumigatus</i> BETA (1-3) GLUCANOSYLTRANSFERASE GEL3P (FRAGMENT).	Cell-Wall	-1,9	-2,1
TREMBL Q07229 <i>Saccharomyces cerevisiae</i> VERPROLIN.	Cell-Wall	-1,9	-31,4
TREMBL Q9P3F4 <i>Neurospora crassa</i> RELATED TO CHITINASE 3 PRECURSOR PROTEIN.	Cell-Wall	-2,2	-2,6
SWISSPROT Q04951 <i>Saccharomyces cerevisiae</i> Probable family 17 glucosidase SCW40 precursor (EC 3.2.1.-)	Cell-Wall	-2,3	1,5
TREMBL AAC49609 <i>Saccharomyces diastaticus</i> Glucoamylase.	Carbon-metabolism	2,5	1,2
TREMBL Q96WT4 <i>Aspergillus oryzae</i> MALTASE	Carbon-metabolism	2,3	5,9
GENESEQP AAW88044 <i>Acremonium</i> sp. An enzyme with sugar transferase activity	Carbon-metabolism	1,9	2,3

Annotation	Pathway	Fold reg day 3	Fold reg day 4
GENESEQP:AA556815 <i>Bacillus</i> sp. <i>Bacillus</i> D-arabinitol dehydrogenase.	Carbon-metabolism	1,9	1,4
TREMBL Q9P8R5 <i>Aspergillus niger</i> D-XYLOSE REDUCTASE.	Carbon-metabolism	1,6	1,6
TREMBL AAM46059 <i>Oryza sativa</i> Putative aldose 1-epimerase-like protein.	Carbon-metabolism	1,6	3,5
SWISSPROT:P50166 <i>Candida tropicalis</i> (EC=1.1.1.250) D-arabinitol 2-dehydrogenase [ribulose forming] (EC 1.1.1.25)	Carbon-metabolism	1,6	2,5
TREMBL Q9TEM3 <i>Emmericella nidulans</i> (EC=4.1.3.31) METHYLCITRATE SYNTHASE PRECURSOR (EC 4.1.3.31).	Carbon-metabolism	1,6	1,4
TREMBL Q9URW9 <i>Schizosaccharomyces pombe</i> PROBABLE ALDEHYDE DEHYDROGENASE.	Carbon-metabolism	1,5	1,2
SWISSPROT:P44538 <i>Haemophilus influenzae</i> (EC=3.5.99.6) Glucosamine-6-phosphate isomerase (EC 3.5.99.6) (Glucosamine	Carbon-metabolism	1,4	3,1
TREMBL CAD36981 <i>Neurospora crassa</i> Related to glucosidase II, alpha subunit.	Carbon-metabolism	1,4	1,8
TREMBL Q9HGZ3 <i>Aspergillus oryzae</i> HEXOKINASE.	Carbon-metabolism	1,4	1,5
GENESEQP:AAR70209 <i>Aspergillus niger</i> A. <i>niger</i> alpha-galactosidase.	Carbon-metabolism	1,3	3,1
TREMBL Q9P8D6 <i>Aspergillus niger</i> (EC=4.1.3.7) CITRATE SYNTHASE PRECURSOR (EC 4.1.3.7).	Carbon-metabolism	-1,2	-1,9
TREMBL Q9HGY8 <i>Aspergillus oryzae</i> (EC=5.3.1.1) TRIOSEPHOSPHATE ISOMERASE (EC 5.3.1.1) (TIM).	Carbon-metabolism	-1,3	-2,8
TREMBL Q9HGY7 <i>Aspergillus oryzae</i> GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE.	Carbon-metabolism	-1,3	-1,8
SWISSPROT:Q12560 <i>Aspergillus oryzae</i> (EC=4.2.1.11) Enolase (EC 4.2.1.11) (2-phosphoglycerate dehydratase) (2-ph	Carbon-metabolism	-1,4	-1,4
TREMBL Q9C415 <i>Aspergillus oryzae</i> (EC=1.2.1.12) GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE (EC 1.2.1.12).	Carbon-metabolism	-1,4	-2,1
SWISSPROT:O13309 <i>Pichia stipitis</i> (EC=1.1.1.1) Alcohol dehydrogenase II (EC 1.1.1.1) (ADH 1).	Carbon-metabolism	-1,4	-1,5
TREMBL Q9C253 <i>Neurospora crassa</i> PROBABLE GLYCERONE KINASE ISOFORM.	Carbon-metabolism	-1,5	-1,3
TREMBL Q9P8D6 <i>Aspergillus niger</i> (EC=4.1.3.7) CITRATE SYNTHASE PRECURSOR (EC 4.1.3.7).	Carbon-metabolism	-1,7	-2,8
TREMBL Q9HE50 <i>Neurospora crassa</i> RELATED TO MALATE DEHYDROGENASE (OXALOACETATE-DECARBOXYLATIN	Carbon-metabolism	-1,8	-1,6
TREMBL O94185 <i>Aspergillus oryzae</i> PYRUVATE DECARBOXYLASE.	Carbon-metabolism	-2,2	-7,3
ERDBP.NP000614 <i>Aspergillus oryzae</i> Deduced amino acid sequence for A <i>oryzae</i> EST AS1789 having h	AO EST	1,6	1,4
ERDBP.NP000292 <i>Aspergillus oryzae</i> Deduced amino acid sequence of genomic DNA sequence encoding	AO EST	-2,3	-3,8